CLAIMS

WE CLAIM

1. A substantially purified EC-3 protein isolated from *E. carinatus* venom, characterized by:

(a) an apparent molecular mass of about 14,762 Da, as determined by electrospray ionization mass spectrometry;

(b) elution from a C-18 HPLC column at about 40% acetonitrile; and

(c) the ability to inhibit adhesion of Jurkat cells to VCAM-1.

2. A substantially purified EC-3A peptide isolated from EC-3 protein which has been reduced and alkylated, characterized by:

(a) a molecular mass of about 8478 Da in its ethylpyridylated form, as determined by electrospray ionization mass spectrometry;

(b) elution from a C-18 HPLC column at about 42% acetonitrile; and

(c) the ability to inhibit adhesion of K562 cells to fibronectin.

3. A substantially purified EC-3B peptide isolated from EC-3 protein which has been reduced and alkylated with vinylpyridine, characterized by:

(a) a molecular mass of about 7950 Da in its carboxymethylated form, as determined by electrospray ionization mass spectrometry;

(b) elution from a C-18 HPLC column at about 46% acetonitrile; and

(c) the ability to inhibit adhesion of Jurkat cells to VCAM-1.

4. A substantially purified EC-3A peptide comprising the sequence SEQ ID NO:19, or a biologically active fragment or derivative thereof.

5. The peptide of claim 4 comprising the sequence SEQ ID NO: 2.

6. A substantially purified EC-3B peptide comprising the sequence SEQ ID NO:20, or a biologically active fragment or derivative thereof.

7. The peptide of claim 6 comprising the sequence SEQ ID NO: 3.

8. A substantially purified EC-3 protein comprising two subunits, wherein one subunit comprises the sequence SEQ ID NO:19 or a biologically active fragment or derivative thereof and one subunit comprises the sequence SEQ ID NO:20 or a biologically active fragment or derivative thereof.

9. A biologically active fragment according to claim 6 having the sequence X-Y-Met-Leu-Asp-Z, where X is H or a blocking group, Y is zero or more amino acids, and Z is OH or zero or more amino acids.

10. A biologically active fragment according to claim 9 wherein said fragment is a peptide having from about 3 to about 20 amino acids.

11. A fragment according to claim 10 having the sequence SEQ ID NO:16.

12. A fragment according to claim 10 having the sequence SEQ ID NO:14.

13. A substantially purified nucleic acid selected from the group consisting of:

(a) nucleic acids encoding the protein or peptide of any of claims 1-12;

(b) nucleic acids hybridizing at high stringency with the nucleic acid in (a); and

(c) nucleic acids derived from (a) or (b) as a result of the degeneracy of the genetic code.

14. A vector comprising the nucleic acid of claim 13.

15. A recombinant cell comprising the nucleic acid of claim 13.

16. An antibody which specifically binds to one of the proteins or peptides of claims 1-12.

17. The antibody of claim 16 wherein said antibody is a monoclonal antibody.

18. A hybridoma that produces the antibody of claim 17.

19. The antibody of claim 16 wherein said antibody is a polyclonal antibody.

20. A substantially purified eichistatin polypeptide in which the Arg-Gly-Asp residues at positions 24-26 are replaced by Met-Leu-Asp, or a biologically active fragment or derivative thereof.

21. A method of isolating a peptide that binds to an integrin of interest from venom comprising:

(a) dissolving venom in a solvent,

(b) centrifuging the dissolved venom to remove high molecular weight proteins,

(c) fractionating the supernatant from step (b),

(d) immobilizing the fractions from step (c) on a solid support,

(e) adding detectably labeled cells that express the integrin of interest to the immobilized fractions,

(f) detecting the number of cells bound to each immobilized fraction, and

(g) isolating peptide from those fractions which showed enhanced cell binding in step (f).

22. A composition comprising a pharmaceutically acceptable carrier and the protein or peptide of any of claims 1-12, or a pharmaceutically acceptable salt thereof.

23. A composition comprising a pharmaceutically acceptable carrier and the nucleic acid of claim 13.

24. A method of inhibiting the binding of an α4 integrin to VCAM-1 comprising contacting a cell that expresses the α4 integrin with an effective amount of a protein or peptide according to one of claims 1-12, or a pharmaceutically acceptable salt thereof.

25. The method of claim 24 wherein the integrin is α4β1 or α4β7.

26. A method of inhibiting the binding of α4β7 integrin to MadCAM-1 comprising contacting a cell that expresses α4β7 with an effective amount of a protein or peptide according to one of claims 1-12, or a pharmaceutically acceptable salt thereof.

27. A method of inhibiting the binding of an α4 integrin to CS-1 comprising contacting a cell that expresses the α4 integrin with an effective amount of a protein or peptide according to one of claims 1-12, or a pharmaceutically acceptable salt thereof.

28. A method of inhibiting the interaction between cells expressing an α4 integrin and VCAM-1 in a patient in need of such treatment comprising administration of a therapeutically effective amount of a composition according to claim 22.

29. A method of inhibiting the interaction between cells expressing an α4 integrin and MadCAM-1 in a patient in need of such treatment comprising administration of a therapeutically effective amount of a composition according to claim 22.

30. A method of inhibiting the interaction between cells expressing an α4 integrin and CS-1 in a patient in need of such treatment comprising administration of a therapeutically effective amount of a composition according to claim 22.

31. A substantially purified EC-3A peptide characterized by:

(a) a sequence having substantial homology with SEQ ID NO:2; and

(b) the ability to inhibit adhesion of K562 cells to fibronectin.

32. A substantially purified EC-3B peptide characterized by:

(a) a sequence having substantial homology with SEQ ID NO:3; and

(b) the ability to inhibit adhesion of Jurkat cells to VCAM-1.

33. A substantially purified nucleic acid selected from the group consisting of:

(a) nucleic acids encoding the peptide of claims 31 or 32;

(b) nucleic acids hybridizing at high stringency with the nucleic acid in (a); and

(c) nucleic acids derived from (a) or (b) as a result of the degeneracy of the genetic code.